SEQUENCE LISTING

<110> KUSUNOKI, CHIHIRO FUKUSHIMA, ATSUSHI

<120> METHOD FOR PREPARING MONOCLONAL ANTIBODY

<130> SHIM-013

<150> JP11-087929 <151> 1999-03-30

<150> JP00/02022 <151> 2000-03-30

<160> 5

<170> PatentIn Ver. 2.1

<210> 1 <211> 1507

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (12)..(1400)

<400> 1

gaattegget t atg aaa eac etg tgg tte tte etc etc etg gtg gea get Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala

98 ccc aga tgg gtc ctg tcc cag gtt cag cta cag cag tgg ggc gca gga Pro Arg Trp Val Leu Ser Gln Val Gln Leu Gln Gln Trp Gly Ala Gly 15

ctg ttg aag cct tcg gag acc ctg tcc ctc acc tgc gct gtc tat ggt 146 Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly

ggg tcc ttc agt ggt tac tac tgg acc tgg atc cgc cag ccc cca ggg Gly Ser Phe Ser Gly Tyr Tyr Trp Thr Trp Ile Arg Gln Pro Pro Gly 50

aag ggg ctg gag tgg att ggg gaa atc att cat cat gga aac acc aac 242 Lys Gly Leu Glu Trp Ile Gly Glu Ile Ile His His Gly Asn Thr Asn 70

tac aac ccg tcc ctc aag agt cga gtc tcc ata tca gtt gac acg tcc 290 Tyr Asn Pro Ser Leu Lys Ser Arq Val Ser Ile Ser Val Asp Thr Ser 80

aaq aac caq ttc tcc ctg aca ctq aqc tct qtg acc gcc gcg gac acg 338 Lys Asn Gln Phe Ser Leu Thr Leu Ser Ser Val Thr Ala Ala Asp Thr 95 100

gct gtg tat tac tgt gcg aga ggg gga gca gtg gct gcg ttt gac tac 386 Ala Val Tyr Tyr Cys Ala Arg Gly Gly Ala Val Ala Ala Phe Asp Tyr 110 115 120

a Pro Pro Val Ala Gly Pro 250 g gac acc ctc atg atc tcc 818 s Asp Thr Leu Met Ile Ser 265 g gac gtg agc cac gaa gac 866 l Asp Val Ser His Glu Asp 280 c ggc gtg gag gtg cat aat 914 p Gly Val Glu Val His Asn	a Pro Pro Val Ala Gly Pro 250 g gac acc ctc atg atc tcc 818 s Asp Thr Leu Met Ile Ser 265 g gac gtg agc cac gaa gac 866 l Asp Val Ser His Glu Asp 280 c ggc gtg gag gtg cat aat 914 p Gly Val Glu Val His Asn 5 acc aac agc acg ttc cgt gtg 962	Ala Pro Pro Val Ala Gly Pro 250 aag gac acc ctc atg atc tcc 818 Lys Asp Thr Leu Met Ile Ser 265 gtg gac gtg agc cac gaa gac 866 Val Asp Val Ser His Glu Asp 280 gac ggc gtg gag gtg cat aat 914 Asp Gly Val Glu Val His Asn 295 ttc aac agc acg ttc cgt gtg Phe Asn Ser Thr Phe Arg Val
Pro Pro Val Ala Gly Pro 250 gac acc ctc atg atc tcc 818 asp Thr Leu Met Ile Ser 265 gac gtg agc cac gaa gac 866 asp Val Ser His Glu Asp 285 ggc gtg gag gtg cat aat 914 Gly Val Glu Val His Asn	Pro Pro Val Ala Gly Pro 250 gac acc ctc atg atc tcc 818 gac gtg agc cac gaa gac 866 gac gtg agc cac gaa gac 866 ggc gtg gag gtg cat aat 914 Gly Val Glu Val His Asn 300 gac agc acg ttc cgt gtg 962 Asn Ser Thr Phe Arg Val	Pro Pro Val Ala Gly Pro 250 gac acc ctc atg atc tcc ssp Thr Leu Met Ile Ser 265 gac gtg agc cac gaa gac ssp Val Ser His Glu Asp 285 ggc gtg gag gtg cat aat sly Val Glu Val His Asn 300 gac acc acg ttc cgt gtg ssp Val Ser Thr Phe Arg Sly Val Ser Gly Lys Glu 330 gac acc ccc atc gag aaa Ser Ala Pro Ile Glu Lys 345 gaa cca cag gtg tac acc Slu Pro Gln Val Tyr Thr
s Asp Thr Leu Met Ile Ser 265 g gac gtg agc cac gaa gac 866 l Asp Val Ser His Glu Asp 280 285 c ggc gtg gag gtg cat aat 914 p Gly Val Glu Val His Asn	s Asp Thr Leu Met Ile Ser 265 g gac gtg agc cac gaa gac 866 l Asp Val Ser His Glu Asp 280 c ggc gtg gag gtg cat aat 914 p Gly Val Glu Val His Asn 5 300 c aac agc acg ttc cgt gtg 962 e Asn Ser Thr Phe Arg Val	Lys Asp Thr Leu Met Ile Ser 265 gtg gac gtg agc cac gaa gac 866 Val Asp Val Ser His Glu Asp 280 gac ggc gtg gag gtg cat aat 914 Asp Gly Val Glu Val His Asn 295 ttc aac agc acg ttc cgt gtg 962 Phe Asn Ser Thr Phe Arg Val 315 gac tgg ctg aac ggc aag gag 1010 Asp Trp Leu Asn Gly Lys Glu 330 ctc cca gcc ccc atc gag aaa 1058 Leu Pro Ala Pro Ile Glu Lys 345 cga gaa cca cag gtg tac acc 1106 Arg Glu Pro Gln Val Tyr Thr
Asp Val Ser His Glu Asp 280 285 c ggc gtg gag gtg cat aat 914 p Gly Val Glu Val His Asn	1 Asp Val Ser His Glu Asp 280 c ggc gtg gag gtg cat aat p Gly Val Glu Val His Asn 5 aac agc acg ttc cgt gtg e Asn Ser Thr Phe Arg Val	Val Asp Val Ser His Glu Asp 280 gac ggc gtg gag gtg cat aat Asp Gly Val Glu Val His Asn 295 ttc aac agc acg ttc cgt gtg Phe Asn Ser Thr Phe Arg Val 315 gac tgg ctg aac ggc aag gag Asp Trp Leu Asn Gly Lys Glu 330 ctc cca gcc ccc atc gag aaa Leu Pro Ala Pro Ile Glu Lys 345 cga gaa cca cag gtg tac acc Arg Glu Pro Gln Val Tyr Thr
o Gly Val Glu Val His Asn	c aac agc acg ttc cgt gtg 962 Asn Ser Thr Phe Arg Val	c aac agc acg ttc cgt gtg 962 c Asn Ser Thr Phe Arg Val 315 c tgg ctg aac ggc aag gag 1010 c Trp Leu Asn Gly Lys Glu 330 c cca gcc ccc atc gag aaa 1058 c Pro Ala Pro Ile Glu Lys 345 c gaa cca cag gtg tac acc 1106 c Glu Pro Gln Val Tyr Thr
	Asn Ser Thr Phe Arg Val	Asn Ser Thr Phe Arg Val 315 tgg ctg aac ggc aag gag 1010 Trp Leu Asn Gly Lys Glu 330 cca gcc ccc atc gag aaa 1058 Pro Ala Pro Ile Glu Lys 345 gaa cca cag gtg tac acc 1106 Glu Pro Gln Val Tyr Thr
Trp Leu Asn Gly Lys Glu		Glu Pro Gln Val Tyr Thr
p Trp Leu Asn Gly Lys Glu 330 c cca gcc ccc atc gag aaa 1058 u Pro Ala Pro Ile Glu Lys	u Pro Ala Pro Ile Glu Lys	

370 375 380

tgc Cys					ttc Phe											1202
agc Ser	aat Asn	ggg Gly 400	cag Gln	ccg Pro	gag Glu	aac Asn	aac Asn 405	tac Tyr	aag Lys	acc Thr	aca Thr	cct Pro 410	ccc Pro	atg Met	ctg Leu	1250
gac Asp																1298
					ggg Gly 435											1346
gct Ala					tac Tyr											1394
aaa Lys	tga	gtgo	ccaco	ggc (eggea	agco	cc co	egeto	ccca	a ggo	ctcto	eggg	gtc	gagt	gag	1450
gatg	ıctt	ggc a	acgta	accc	eg to	gtaca	atact	t to	ccag	gcac	cca	gcaaa	agc (cgaat	tc	1507
<210 <211	> 46															
<212 <213		omo s	sapie	ens												
<213 <400	3> Ho 3> 2	omo s	_		Phe	Phe	Leu	Leu	Leu 10	Val	Ala	Ala	Pro	Arg 15	Trp	
<213 <400 Met	3> Ho 3> 2 Lys	omo s	Leu	Trp 5					10					15		
<213 <400 Met 1 Val	3> Ho 3> 2 Lys Leu	His Ser	Leu Gln 20	Trp 5 Val		Leu	Gln	Gln 25	10 Trp	Gly	Ala	Gly	Leu 30	15 Leu	Lys	
<213 <400 Met 1 Val	3> Ho 0> 2 Lys Leu Ser	His Ser Glu 35	Leu Gln 20 Thr	Trp 5 Val Leu	Gln	Leu Leu	Gln Thr 40	Gln 25 Cys	10 Trp Ala	Gly Val	Ala Tyr	Gly Gly 45	Leu 30 Gly	15 Leu Ser	Lys Phe	
<213 <400 Met 1 Val Pro	3> Ho 0> 2 Lys Leu Ser Gly 50	His Ser Glu 35	Leu Gln 20 Thr	Trp 5 Val Leu Trp	Gln Ser	Leu Leu Trp 55	Gln Thr 40	Gln 25 Cys Arg	10 Trp Ala Gln	Gly Val Pro	Ala Tyr Pro 60	Gly Gly 45 Gly	Leu 30 Gly Lys	15 Leu Ser Gly	Lys Phe Leu	
<213 <400 Met 1 Val Pro Ser Glu 65	3> Ho 3> 2 Lys Leu Ser Gly 50	His Ser Glu 35 Tyr	Leu Gln 20 Thr Tyr	Trp 5 Val Leu Trp	Gln Ser Thr	Leu Leu Trp 55	Gln Thr 40 Ile	Gln 25 Cys Arg	Trp Ala Gln Gly	Gly Val Pro Asn 75	Ala Tyr Pro 60 Thr	Gly 45 Gly Asn	Leu 30 Gly Lys	15 Leu Ser Gly Asn	Lys Phe Leu Pro 80	
<213 <400 Met 1 Val Pro Ser Glu 65 Ser	3> Ho 3> 2 Lys Leu Ser Gly 50 Trp Leu	His Ser Glu 35 Tyr Ile	Leu Gln 20 Thr Tyr Gly Ser	Trp 5 Val Leu Trp Glu Arg 85	Gln Ser Thr Ile 70	Leu Trp 55 Ile Ser	Gln Thr 40 Ile His	Gln 25 Cys Arg His	Trp Ala Gln Gly Val 90	Gly Val Pro Asn 75 Asp	Ala Tyr Pro 60 Thr	Gly 45 Gly Asn Ser	Leu 30 Gly Lys Tyr	15 Leu Ser Gly Asn Asn	Lys Phe Leu Pro 80 Gln	
<213 <400 Met 1 Val Pro Ser Glu 65 Ser	S> Ho D> 2 Lys Leu Ser Gly 50 Trp Leu Ser	His Ser Glu 35 Tyr Ile Lys Leu	Leu Gln 20 Thr Tyr Gly Ser Thr 100	Trp 5 Val Leu Trp Glu Arg 85 Leu	Gln Ser Thr Ile 70 Val	Leu Trp 55 Ile Ser	Gln Thr 40 Ile His Ile Val	Gln 25 Cys Arg His Ser	Trp Ala Gln Gly Val 90 Ala	Gly Val Pro Asn 75 Asp	Ala Tyr Pro 60 Thr Thr	Gly 45 Gly Asn Ser	Leu 30 Gly Lys Tyr Lys Ala 110	15 Leu Ser Gly Asn Asn 95 Val	Lys Phe Leu Pro 80 Gln Tyr	

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser 165 170 175

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val 180 185 190

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro 195 200 205

Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys 210 215 220

Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val 225 230 235 240

Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe 245 250 255

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro 260 265 270

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val 275 280 285

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr 290 295 300

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val 305 310 315 320

Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys 325 330 335

Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser 340 345 350

Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro 355 360 365

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val 370 380

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly 385 390 395 400

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp 405 410 415

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp 420 425 430

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His 435 440 445

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys 450 455 460

<210> 3 <211> 23

<212> DNA <213> Artificial Sequ	ence	
	Artificial Sequence: Artificially mer sequence, HG2-3-437	
<400> 3 gtgtaggtct gggtgccgaa	gtt 2	23
<210> 4 <211> 23 <212> DNA <213> Artificial Sequ	ence	
_	Artificial Sequence:Artificially mer sequence, VH4-21	
<400> 4 atgaaacacc tgtggttctt	cct 2	23
<210> 5 <211> 23 <212> DNA <213> Artificial Sequ	ence	
_	Artificial Sequence:Artificially mer sequence, CG2-1	
<400> 5 gctgggtgcc tgggaagtat	gta 2	23